Conclusion: Because molecular typing makes it possible to track the dissemination of specific clones, it may facilitate the breaking down of endemic transmission to the level of micro-epidemics.

MoG2-3 Is multi-resistance an indicator of higher transmissibility of nosocomial pathogens?

M. J. Struelens
Université Libre de Bruxelles, Hopital Erasme, Brussels, Belgium

A large number of molecular epidemiologic studies document the epidemic spread of antibiotic-resistant clones of nosocomial pathogens within and between hospitals. The pressure of intense antibiotic use in the hospital patient population confers a selective advantage to resistant clones which are more likely to survive and multiply to replace the antibiotic susceptible commensal flora. Examples of epidemic antibiotic resistant clones associated with large scale epidemics which can lead to a net excess of nosocomial infection by that species include methicillin-resistant *Staphylococcus aureus*, clindamycin-resistant *Clostridium difficile*, multi-drug resistant *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Enterobacter aerogenes* and *Burkholderia cepacia*. Less information is available regarding the hypothesis that successful antibiotic resistant clones carry additional virulence determinants enhancing their transmissibility and/or pathogenicity. This type of association has been found among epidemic types of *Klebsiella pneumoniae*, carrying large plasmids encoding multi-drug resistance (extended spectrum beta-lactamase, aminoglycoside modifying enzymes) aerobactin and an adhesin promoting colonization of intestinal epithelium. Likewise, a pandemic electrophoretype 12 of *Burkholderia cepacia* associated with nosocomial outbreaks in cystic fibrosis patients harbours a specific gene coding for the *cblA* pilin subunit and a conserved IS element which may promote genomic rearrangements involved in resistance or transmissibility. Whereas multi-resistance is often an indicator of epidemicity for nosocomial pathogens, more studies are needed to determine genetic and functional determinants of enhanced transmissibility of epidemic clones beyond the selective advantage of resistance. Identification of such markers would be useful to predict the epidemic potential of clinical isolates and respond accordingly with infection control measures.

MoG2-5 What tools do we need to understand the dynamics of hospital acquired infections in places like intensive care units?

Hajo Grundmann
Nottingham, United Kingdom University

Molecular typing provides infection control personnel with a wealth of data pertaining to the population structure of the pathogens that are isolated from patients. Since hospital epidemiologists are conventionally more interested in the population of hosts than in that of the pathogens routine typing data are usually not exploited to their full potential. Using this data for the analysis of time space interaction by genotype may lead to the identification of miniclusters that occur above a certain level of expectancy. A couple of statistical tests can be employed to that end. Another way of utilising typing data introduces differential risk factor analysis which may include some classical case control or cohort approaches. In typically endemic situations i.e in the absence of outbreaks, hidden transmission dynamics may thus be revealed and the success of preventive measures may be predicted by simple stochastic models.

SG03 – ESGNI

MoG3-1 Diagnosis and prevention of surgical site infections: Problems with definitions

R. C. Spencer
Public Health Laboratory, Bristol BS2 8HW, United Kingdom

Surveillance studies require careful planning with a clear protocol, but, above all, they need accepted definitions. No single set of definitions has been universally adopted, although there is a generally agreed-upon group of ideas or problems central to the issue. A variety of definitions of nosocomial infections have been proposed and used in hospital surveillance studies. Some reports have proposed very simple definitions, while others have produced much more detailed ones. Even when epidemiologists, nurses and clinical microbiologists have produced consensus definitions, some health-care workers still find problems in their interpretation. There is no doubting that variations in definitions can influence the recorded rate of infection and without definitive definitions, comparisons between hospitals are meaningless. Unfortunately many individual institutions modify these consensus definitions to suit their own particular resident populations and doctor/laboratory facilities and availability. Indeed, some authors recommend that this should happen. Whichever definitions are used, microbiological and imaging findings should be used only to confirm clinical evidence of infection. It is strongly recommended that all professional associations of those health-care workers involved in the surveillance of nosocomial infections should co-operate to develop standardised case definitions suitable for routine use. A plea is made for simplicity and clarity. It remains essential that such case definitions for surveillance purposes ensure a high level of sensitivity in order to allow the earliest detection of infective nosocomial problems.

MoG3-2 Nosocomial aspergillosis: Are there effective measures for prevention

Patricia Muñoz
Hospital General Universitario "Gregorio Marañon", Madrid, Spain

Aspergillosis is the second most common nosocomial mycosis. Recommendations to prevent aspergillosis in high-risk patients include the reduction of environmental exposure and the recognition of predisposing factors and periods of increased risk The strict observation of infection control measures (air quality, isolation of construction works) in centers with immunocompromised patients is essential. Environmental protection trying to insure that the air of selected units is free from *Aspergillus* spores is the most important step of prophylaxis, although it is not always possible. Constant environmental surveillance is a difficult goal and exposure may occur at other sites of the hospital or in the community. The prompt recognition of nosocomial cases is also recommended. The reduction of predisposing factors in high-risk patients may include the prevention and adequate management of neutropenia and rejection episodes, the prevention of infections such as CMV. HHV-6 or relapsing HCV and the judicious use of Immuno suppressive therapy. Targeted surveillance cultures and primary prophylaxis against invasive aspergillosis are not standard measures in solid organ transplant recipients although they are more commonly used for neutropenic patients. The current lack of reliable preventive regimens against aspergillosis and against emerging resistant fungal pathogens presents an ongoing challenge. New antifungal agents, such as triazoles and new AMB presentations, have proved to be useful in some recent studies.

SG04 – EHPSG

MoG4-1 Non-invasive tests for the diagnosis of *Helicobacter pylori* infection

H. Rautelin
Department of Bacteriology and Immunology, Haartman Institute, University of Helsinki, and Helsinki University Central Hospital Laboratory Diagnostics, Helsinki, Finland

Non-invasive (gastroscopy not needed) diagnosis of *H. pylori* infection includes in practice detection of *H. pylori* antibodies, urea breath tests, and a recently developed test detecting *H. pylori* antigen in stool. In the primary diagnosis of *H. pylori* infection, non-invasive diagnostic methods may be used solely in younger patients who are not endoscopied. Among patients endoscopied, non-invasive diagnostic methods are useful in addition to invasive tests. For instance in atrophic gastritis, invasive diagnostic methods, and even urea breath test, may fail in showing *H. pylori* probably due to the low number of bacteria present. However, elevated antibody titres of *H. pylori* may still indicate the infection in these cases. In general, no single test is optimal in the diagnosis of *H. pylori* infection but the best test(s) in each clinical setting may be chosen if the advantages and restrictions of the different tests are known. All diagnostic tests should be validated locally. As the prevalence of *H. pylori* infection is rapidly decreasing in developed countries, the positive predictive value of the test might be very different from that in a high prevalence population.

In contrast to biopsy-based tests, non-invasive diagnostic methods may also be used for the follow-up of eradication therapy; urea breath test as early as 4 weeks and quantitative serology 4–6 months after the therapy. If serology is used for the follow-up, pre-treatment serum sample must be.

MoG4-3 Antimicrobial resistance in *Helicobacter pylori*. The European scene

F. Mégraud
Laboratoire de Bactériologie, Hôpital Pellegrin, Bordeaux, France

Antimicrobial resistance is considered to be the major risk factor for failure of therapies aiming to eradicate *Helicobacter pylori*. In Europe, there is a great diversity in the policies concerning the use of antibiotics. This diversity may be reflected in the resistance rate of *H. pylori*.

A large European survey conducted by Glupczynski *et al.* in 1997–98 involved 22 centers in 17 countries; 1,305 isolates were tested (mean no./center: 59) using a standardized Etest methodology. While the global rate of resistance to clarithromycin was 9.8% [95% CI (8.3–11.5)], there were important variations between the northern (4.5%) and the southern (18.1%) parts of the continent, and between children and adult patients. For metronidazole, the global rate of resistance was 33% [95% CI (30.5–35.6)] with no major regional differences. The drawback of this study, as for many others, is that only referral centers were involved, with a risk of recruitment bias. For this reason, we began an active survey in France where a large number of gastroenterologists were asked to send one positive biopsy on a given day. In 1997, the rate of resistance to clarithromycin was 14%, and to metronidazole 24% (N = 525 adults). It has not increased significantly these last years. A similar survey, but only hospital based, was carried out in Portugal in 1999. The rate of resistance to clarithromycin was 11.6% and to metronidazole 14.3% (N = 545). In northern and central Italy, 200 strains obtained during a clinical trial in DU patients showed a resistance rate of 11.3% to clarithromycin and 14.7% to metronidazole.

Globally, a trend towards increased resistance can be observed for macrolide resistance. While amoxicillin resistance seems uncommon, a strain has been found in the Netherlands, and tolerant strains have been reported in Italy. These results are arguments for setting up surveillance systems in the different European countries.

SG06 – ESGAP

MoG6-2 National antibiotic policies in different CEE countries

V. Krcmery, Jr
School of Public Health, University of Trnava, Trnava, Slovakia; School of Health Administration, University of Scranton, Scranton, PA, United States

Objectives: Increasing consumption of antimicrobial agents and increasing antibiotic resistance in Central Eastern Europe led to a concern of treat Health Care antibiotics. Therefore most of 11 surveyed CEE countries adopted after initial liberalization, all countries included both, national and hospital based antibiotic policies, including antibiotic cauntees, National Hospital ATB formularies, restricted prescribing, HMO/Hospital reserved antibiotics.

Results: Similarities and differences in CEE countries (Slovak Republic, Czech Republic, Hungary, Austria, Germany, Poland, Croatia, Slovenia, etc.) are discussed as well as adherence to various guidelines and their impact to ATB consumption. Four of 11 countries has centralized but 9 of 11 hospital based ATB policies. Numerous antimicrobials are restricted in 8 of 11 countries for hospital use. However, only 3 of 11 CEE countries restrict ATB (e.g. qiunolones of 3rd Generation CEF's) for GP use.

SG07 – ESGMD

TuG7-3 Molecular detection of antibiotic resistance

R. Leclercq
Microbiology, CHU Caen, 14033 Caen cedex, France

A major research effort in clinical microbiology has been the development of rapid methods for antimicrobial susceptibility testing. The genotypic approach could offer interesting possibilities to detect antimicrobial resistances since it is rapid and independent from breakpoint categorization which differs from a country, to another one. DNA probes, including oligonucleotide probes, were first used for detection of resistance genes. Nucleic acid-based amplification techniques have been developped which improve sensitivity of detection and allows detection of resistance directly from clinical samples. Recently developped methods, DNA chips, would allow to use thousands of oligonucleotides in a single reaction. One possible limitation of these techniques is the observation that not only acquisition or mutation of structural genes are responsible for resistance, but also regulation of gene expression. Also, false positive results are expected in the case of silent genes detected by the genotypic techniques but not expressed.

Applications are mostly developped for resistances difficult to detect phenotypically in rapidly growing bacteria, such as methicillin resistance in staphylococci or glycopeptide resistance in enterococci, or resistance in fastidious organisms, such as mycobacteria and *Helicobacter pylori*. In the latter case, resistances can be detected by PCR done on bacterial DNA extracted from gastric biopsy material.

Synergistic combination of genotypic and phenotypic techniques should help to rule out inappropriate therapy. The genotypic approach could help the physicians to prescribe antibiotics only to patients who need them. Information provided by the genotypic techniques should help to evaluate the extent of the resistance determinant pool in outbreaks.

SG10 – EWPARAB

TuG10-1 Taxonomy of new anaerobic bacteria

Hannele Jousimies-Somer
National Public Health Institute, Helsinki, Finland

As a result of 16S rRNA sequencing, major reorganizations among anaerobic taxa are underway. The gram-negative pigmented *Prevotella* now include 8 species, the latest being *Pr. nigrescens*, *Pr. tannerae* and *Pr. pallens*, The nonpigmented former *Mitsuokella dentalis* and *Hallella seregens* were renamed as one species, *Prevotella dentalis*. The bile-sensitive, oral *Pr. heparinolytica* and *Pr. zoogleoformans* phylogene- tically cluster in *B. fragilis*-group. *Bacteroides tectum* homology group II (zoonotic) are genotypically identical with *B. pyogenes*. The bile-resistant *B. distasonis* clusters with *B. forsythus* among *Porphyromonas* which currently include 11 pigmented and one nonpigmented species: *P. catoniae;* several new groups awaite inclusion. *Fusobacterium nucleatum* currently has 5 subspecies and is very heterogenous; (phylo)genetic analyses place *F. periodonticum* within *F. nucleatum*. *F. varium* includes *F. pseudonecrophorum*. The bile-sensitive, former *B. gracilis* now are *Campylobacter gracilis;* the bile-resistant variants belog to a new genus *Sutterella* as *S. wadsworthensis*. *Capnocytophaga hemolytica*, *C. granulosa* and *Leptotrichia sanquinegens* are new species among the capnophilic taxa. *Desulfovibrio fairfieldensis* is a new species among the *Desulfovibrio* and *Anaerobiospirillum thomasii* a new spiral, motile organism.

The new *Actinomyces* species include two subspecies of *A. neuii*, *A. radingae* - *A. turicensis* complex, *A. europaeus*, *A. slackii*, *A. graevenitzii* and several other species. *A. pyogenes* and *A. bernardiae* were recently transferred to the genus *Arcanobacterium*. *Actinomyces suis* and *Actinomyces*-like organisms from human origin were reclassified to a new genus *Actinobaculum*. The genus *Eubacterium* sensu stricto is represented by *E. limosum* and the former *E. alactolyticum* was reclassified in a new genus *Pseudoramibacter* as *P. alactolyticus*. *Eggerthella lenta* was *Eubacterium lentum;* other new gram-positive genera include *Collinsella*, *Slackia*, *Crypto bacterium*, *Atopobium*, *Holdemania* and *Filifactor*. The genus *Peptostreptococcus* also harbors new species; *P. harei*, *P. ivorii* and *P. octavius*. *Finegoldia magnus* and *Micromonas micros* are new synonyms of *P. magnus* and *P. micros*, respectively.

TuG10-3 Antibiotic susceptibility of *Bacteroides fragilis* in Europe

E. Nagy
Dept. of Clinical Microbiology, Faculty of Medicine, University of Szeged, Hungary

Bacteroides fragilis is the most commonly isolated human pathogenic anaerobic bacterium belonging in the *Bacteroides* genus, *senso stricto*. Antibiotic resistance problems were reported most frequently for members of this genus during past decades, often without discrimination of isolates on a species level. Besides the reference agar-dilution method, the determination of MICs by the Etest has become available for routine laboratories to evaluate the resistance of clinical isolates of anaerobes more easily.

Antibiotic resistance due to beta-lactamase activity is observed most oftenamong *B. fragilis* and related species. A unique metallo-beta-lactamase production of *B. fragilis* is responsible for the resistance of this species to carbapenems. The presence of the *cfi*A gene, coding the production of this enzyme, hes been detected by PCR among carbapenem-resistant and susceptible strains in different parts of Europe. The expression of the *cfi*A gene was found to be connected with the presence of IS elements. Decreased